

SEQUENCE LISTING

<110> Biemans, Ralph
 Denoel, Philippe
 Feron, Christiane
 Goraj, Karine
 Kortekaas, Jeroen
 Poolman, Jan
 Tommassen, Jan
 Weynants, Vincent

<120> Mutant Protein and Refolding Method

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<213> Neisseria meningitidis

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<213> Neisseria gonorrhoeae

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<213> Neisseria gonorrhoeae

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<212> DNA

<213> Neisseria meningitidis

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<210> 8

<211> 697

<212> PRT

<213> *Neisseria meningitidis*

<400> 8

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Lys Asp Glu Ser Thr Ala Thr Asp Met Arg Glu Leu Leu Lys Glu Glu
 35          40          45
Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly Thr Ser Gln Phe Leu Thr
 50          55          60
Leu Arg Gly Met Gly Gln Asn Ser Val Asp Ile Lys Val Asp Asn Ala
 65          70          75          80
Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln Gly Arg Phe Ile Val Asp
 85          90          95
Pro Ala Leu Val Lys Val Val Ser Val Gln Lys Gly Ala Gly Ser Ala
100          105          110
Ser Ala Gly Ile Gly Ala Thr Asn Gly Ala Ile Ile Val Lys Thr Val
115          120          125
Asp Gly Gln Asp Leu Leu Lys Gly Leu Asp Lys Asn Trp Gly Val Arg
130          135          140
Leu Asn Ser Gly Phe Ala Ser Asn Glu Gly Val Ser Tyr Gly Ala Ser
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Val Phe Gly Lys Glu Gly Asn Phe Asp Gly Leu Phe Ser Tyr Asn Arg
165          170          175
Asn Asp Glu Lys Asp Tyr Glu Ala Gly Lys Gly Phe Arg Asn Val Thr
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Gly Gly Lys Thr Val Pro Tyr Ser Ala Leu Asp Lys Arg Ser Tyr Leu
195          200          205
Ala Lys Ile Gly Thr Ser Phe Gly Gly Asp Asp His Arg Ile Val Leu
210          215          220
Ser His Met Lys Asp Gln His Arg Gly Ile Arg Thr Val Gly Glu Glu
225          230          235          240

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Pro	His	Ser	Gln	Arg	Trp	Thr	Asn	Thr	Leu	Pro	Asp	Val	Gly	Arg	Asp	
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<211> 2123
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 <213> Neisseria meningitidis

<400> 9

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<210> 10
 <211> 692
 <212> PRT
 <213> Neisseria meningitidis

<400> 10

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 20          25          30
Lys Asp Glu Ser Thr Ala Thr Asp Met Arg Glu Leu Leu Lys Glu Glu
 35          40          45
Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly Thr Ser Gln Phe Leu Thr
 50          55          60
Leu Arg Gly Met Gly Gln Asn Ser Val Asp Ile Lys Val Asp Asn Ala
 65          70          75          80
Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln Gly Arg Phe Ile Val Asp
 85          90          95
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Leu	Asn	Ser	Pro	Ser	Asp	Ser	Asn	Glu	Gly	Val	Ser	Tyr	Gly	Ala	Ser	145	150	155
Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly	Leu	Phe	Ser	Tyr	Asn	Arg	165	170	175
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Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Gly	Asp	His	Arg	Ile	Val	210	215	220
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Glu	Phe	Thr	Val	Gly	Ala	Lys	Asp	Ser	Arg	Ile	Asn	Ile	Lys	Arg	Gln	245	250	255
Val	Pro	Ala	Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn	Thr	Asn	Leu	Ala	Tyr	260	265	270
Thr	Gly	Lys	Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu	Asp	Ala	Asn	Ala	Tyr	275	280	285
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Tyr	Gly	Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys	Pro	Gln	Ala	Phe	Leu	340	345	350
Asn	Ser	Gln	Phe	Lys	Ile	Glu	Asp	Lys	Glu	Lys	Ala	Thr	Asp	Glu	Glu	355	360	365
Lys	Asn	Lys	Asn	Arg	Glu	Asn	Glu	Lys	Ile	Ala	Lys	Ala	Tyr	Arg	Leu	370	375	380
Thr	Asn	Pro	Thr	Lys	Thr	Asp	Ala	Gly	Ala	Tyr	Ile	Glu	Ala	Ile	His	385	390	395
Glu	Ile	Asp	Gly	Phe	Thr	Leu	Thr	Gly	Gly	Leu	Arg	Tyr	Asp	Arg	Phe	405	410	415
Lys	Val	Lys	Thr	His	Asp	Gly	Lys	Thr	Val	Ser	Ser	Ser	Asn	Leu	Asn	420	425	430
Pro	Ser	Phe	Gly	Val	Ile	Trp	Gln	Pro	His	Glu	His	Trp	Ser	Phe	Ser	435	440	445
Ala	Ser	His	Asn	Tyr	Ala	Ser	Arg	Ser	Pro	Arg	Leu	Tyr	Asp	Ala	Leu	450	455	460
Gln	Thr	His	Gly	Lys	Arg	Gly	Ile	Ile	Ser	Ile	Ala	Asp	Gly	Thr	Lys	465	470	475
Ala	Glu	Arg	Ala	Arg	Asn	Thr	Glu	Ile	Gly	Phe	Asn	Tyr	Asn	Asp	Gly	485	490	495
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Leu	Ala	Asn	Pro	Gln	Asn	Arg	His	Asp	Ser	Val	Ala	Val	Arg	Glu	Ala	515	520	525
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Pro	Arg	Phe	Tyr	Asp	Thr	His	Lys	Asp	Lys	Leu	Leu	Ser	Ala	Asn	Pro	565	570	575
Glu	Phe	Gly	Ala	Gln	Val	Gly	Arg	Thr	Trp	Thr	Ala	Ser	Leu	Ala	Tyr			

			580					585					590				
Arg	Phe	Gln	Asn	Pro	Asn	Leu	Glu	Ile	Gly	Trp	Arg	Gly	Arg	Tyr	Val		
		595						600				605					
Gln	Lys	Ala	Val	Gly	Ser	Ile	Leu	Val	Ala	Gly	Gln	Lys	Asp	Arg	Asn		
	610					615					620						
Gly	Lys	Leu	Glu	Asn	Val	Val	Arg	Lys	Gly	Phe	Gly	Val	Asn	Asp	Ile		
625				630					635						640		
Phe	Ala	Asn	Trp	Lys	Pro	Leu	Gly	Lys	Asp	Thr	Leu	Asn	Val	Asn	Leu		
			645						650					655			
Ser	Val	Asn	Asn	Val	Phe	Asn	Thr	Phe	Tyr	Tyr	Pro	His	Ser	Gln	Arg		
		660						665					670				
Trp	Thr	Asn	Thr	Leu	Pro	Asp	Val	Gly	Arg	Asp	Val	Arg	Leu	Gly	Val		
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Asn	Tyr	Lys	Phe														
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 <212> PRT
 <213> Neisseria gonorrhoeae

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 <211> 23
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 <213> Neisseria meningitidis

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<210> 15
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<213> Neisseria meningitidis

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<210> 18
<211> 29
<212> PRT
<213> Neisseria meningitidis

<400> 18
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<210> 19
<211> 27
<212> PRT
<213> Neisseria meningitidis

<400> 19
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<210> 20

<211> 28
<212> PRT
<213> Neisseria meningitidis

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<210> 21
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<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat domain of repeat toxin

<221> VARIANT
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<223> Xaa = Any Amino Acid

<400> 21
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<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
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<223> Xaa = Any Amino Acid

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1 5

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polymyxin B mimotope

<400> 23
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<210> 24
<211> 10
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<213> Artificial Sequence

<220>

<223> Meningococcal PorA pl.7, 16 loop 4 chimera

<400> 24

Gln Leu Lys Asp Thr Asn Asn Asn Ala Ser
1 5 10

<210> 25

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal PorA pl.7, 16 loop 4 chimera

<400> 25

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<210> 26

<211> 2135

<212> DNA

<213> Artificial Sequence

<220>

<223> Meningococcal frpB with loop 7 deletion

<400> 26

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ggacggcctc ctttgcttac cgcttccaaa atccgaatct ggaaatcggc tggcgcggcc 1860
gttatgttca aaaagctacg ggttcgatat tggcggcagg tcaaaaagac cgcaaaggca 1920
acttgaaaaa cgttgtacgc aaagggttctg gtgtgaacga tgtcttcgcc aactggaaac 1980
cgctgggcaa agacacgctc aatgtcaatc tttcggttaa caacgtgttc aacaagttct 2040
actatccgca cagccaacgc tggaccaata ccctgccggg cgtgggacgt gatgtacgct 2100
tgggcgtgaa ctacaagttc taaaacgcac gacgt 2135

```

<210> 27

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal frpB with loop 7 deletion

<400> 27

```

Met Asn Thr Pro Leu Phe Arg Leu Ser Leu Leu Ser Leu Thr Leu Ala
 1              5              10              15
Ala Gly Phe Ala His Ala Ala Glu Asn Asn Ala Lys Val Val Leu Asp
      20              25              30
Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn
      35              40              45
Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg
 50              55              60
Glu Leu Leu Lys Glu Glu Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly
65              70              75              80
Thr Ser Gln Phe Leu Thr Leu Arg Gly Met Gly Gln Asn Ser Val Asp
      85              90              95
Ile Lys Val Asp Asn Ala Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln
      100             105             110
Gly Arg Phe Ile Val Asp Pro Ala Leu Val Lys Val Val Ser Val Gln
      115             120             125
Lys Gly Ala Gly Ser Ala Ser Ala Gly Ile Gly Ala Thr Asn Gly Ala
130             135             140
Ile Ile Ala Lys Thr Val Asp Ala Gln Asp Leu Leu Lys Gly Leu Asp
145             150             155             160
Lys Asn Trp Gly Val Arg Leu Asn Ser Gly Phe Ala Ser Asn Glu Gly
      165             170             175
Val Ser Tyr Gly Ala Ser Val Phe Gly Lys Glu Gly Asn Phe Asp Gly
      180             185             190
Leu Phe Ser Tyr Asn Arg Asn Asp Glu Lys Asp Tyr Glu Ala Gly Lys
      195             200             205
Gly Phe Arg Asn Val Asn Gly Gly Lys Thr Val Pro Tyr Ser Ala Leu
210             215             220
Asp Lys Arg Ser Tyr Leu Ala Lys Ile Gly Thr Thr Phe Gly Asp Asp
225             230             235             240
Asp His Arg Ile Val Leu Ser His Met Lys Asp Gln His Arg Gly Ile
      245             250             255
Arg Thr Val Arg Glu Glu Phe Thr Val Gly Asp Lys Ser Ser Arg Ile
      260             265             270
Asn Ile Asp Arg Gln Ala Pro Ala Tyr Arg Glu Thr Thr Gln Ser Asn
      275             280             285
Thr Asn Leu Ala Tyr Thr Gly Lys Asn Leu Gly Phe Val Glu Lys Leu
290             295             300
Asp Ala Asn Ala Tyr Val Leu Glu Lys Glu Arg Tyr Ser Ala Asp Asp
305             310             315             320
Ser Gly Thr Gly Tyr Ala Gly Asn Val Lys Gly Pro Asn His Thr Arg
      325             330             335

```



```

tcttaaaaga agagccgtcc atcgatttcg gcggcggcaa cggcacgtcc caattcctga 300
cgctgcgcgg catgggtcag aactctgtcg acatcaaggt ggacaacgcc tattccgaca 360
gccaaatcct ttaccaccaa ggcagattta ttgtcgatcc cgcttttggt aaagtcgttt 420
ccgtacaaaa aggcgcgggt tccgcctctg ccggtatcgg cgcgaccaac ggcgcgatca 480
tcgcaaaaac cgtcgatgcc caagacctgc tcaaaggctt ggataaaaaac tggggcgtgc 540
gcctcaacag cggctttgcc agcaacgaag gcgtaagcta cggcgcaagc gtattcggaa 600
aagagggcaa cttcgacggc ttgttctctt acaaccgcaa cgatgaaaaa gattacgaag 660
ccggcaaagg tttccgcaat gtcaacggcg gcaaaaccgt accgtacagc gcgctggaca 720
aacgcagcta cctcgccaaa atcggaacaa ccttcggcga cgacgaccac cgcctcgtgt 780
tgagccacat gaaagaccgc caagcccctg cttaccgcga aactacccaa tccaacacca 840
acttggcgta cacgggtaaa aacctgggct ttgtcgaaaa actggatgcc aacgcctatg 900
tgttgaaaaa agaacgctat tccgcgatg acagcggcac cggctacgca ggcaatgtaa 960
aaggcccaa ccataccga atcaccactc gtggtgcgaa cttcaacttc gacagccgcc 1020
ttgccgaaca aacctgttg aaatacggta tcaactaccg ccatcaggaa atcaaaccgc 1080
aagcattttt gaactcgaaa ttctccatcc ccgcctacaa actttccaac ccgacaaaaa 1140
ccgataccgg cgtatatgtt gaagccattc acgacatcgg cgatttcacg ctgaccggcg 1200
ggctgcgtta cgaccgcttc aagggtgaaaa cccatgacgg cagaaccgtt tcaagcagca 1260
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gccacaacta cgcagccgc agcccgcgcg tgtatgacgc gctgcaaacc caccgtaaac 1380
gccgcatcat ctcgattgcc gacggcacaa aagccgaacg cgcgcgcaat accgaaatcg 1440
gcttcaacta caacgacggc acgtttgccc caaacggcag ctacttctgg cagaccatca 1500
aagacgcgct tgccaatccg caaaaccgcc acgactctgt cgccgtccgt gaagccgtca 1560
atgccggtta catcaaaaac caccggttac aattgggcgc gtcctaccgc accggcggcc 1620
tgactgccaa agtcggcgtc agccacagca aaccgcgctt ttacgatacg caciaagaca 1680
agctgttgag cgcgaatcct gaatttggcg cacaagtcgg ccgcacttgg accgcctccc 1740
ttgcctaccg cttccaaaat ccgaatctgg aaatcggctg gcgcggccgt tatgttcaaa 1800
aagctacggg ttcgatattg gcggcaggtc aaaaagaccg caaaggcaac ttggaaaacg 1860
ttgtacgcaa aggtttcggg gtgaacgat tcttcgcaa ctggaaaccg ctgggcaaacg 1920
acacgctcaa tgtcaatctt tcggttaaca acgtgttcaa caagttctac tatccgcaca 1980
gccaacgctg gaccaatacc ctgccggggc tgggacgtga tgtacgcttg ggcgtgaact 2040
acaagttcta aaacgcacga cgt 2063

```

<210> 29

<211> 668

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal FrpB with loop 7 and 5 deletion

<400> 29

```

Met Asn Thr Pro Leu Phe Arg Leu Ser Leu Leu Ser Leu Thr Leu Ala
1          5          10          15
Ala Gly Phe Ala His Ala Ala Glu Asn Asn Ala Lys Val Val Leu Asp
20          25          30
Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn
35          40          45
Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg
50          55          60
Glu Leu Leu Lys Glu Glu Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly
65          70          75          80
Thr Ser Gln Phe Leu Thr Leu Arg Gly Met Gly Gln Asn Ser Val Asp
85          90          95
Ile Lys Val Asp Asn Ala Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln
100         105         110
Gly Arg Phe Ile Val Asp Pro Ala Leu Val Lys Val Val Ser Val Gln
115         120         125
Lys Gly Ala Gly Ser Ala Ser Ala Gly Ile Gly Ala Thr Asn Gly Ala
130         135         140
Ile Ile Ala Lys Thr Val Asp Ala Gln Asp Leu Leu Lys Gly Leu Asp

```

145					150					155					160
Lys	Asn	Trp	Gly	Val	Arg	Leu	Asn	Ser	Gly	Phe	Ala	Ser	Asn	Glu	Gly
				165					170					175	
Val	Ser	Tyr	Gly	Ala	Ser	Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly
			180					185					190		
Leu	Phe	Ser	Tyr	Asn	Arg	Asn	Asp	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys
		195					200				205				
Gly	Phe	Arg	Asn	Val	Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu
	210					215				220					
Asp	Lys	Arg	Ser	Tyr	Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Asp
225					230					235					240
Asp	His	Arg	Ile	Val	Leu	Ser	His	Met	Lys	Asp	Arg	Gln	Ala	Pro	Ala
				245					250					255	
Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn	Thr	Asn	Leu	Ala	Tyr	Thr	Gly	Lys
			260					265					270		
Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu	Asp	Ala	Asn	Ala	Tyr	Val	Leu	Glu
		275					280					285			
Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Thr	Gly	Tyr	Ala	Gly	Asn
	290					295					300				
Val	Lys	Gly	Pro	Asn	His	Thr	Arg	Ile	Thr	Thr	Arg	Gly	Ala	Asn	Phe
305					310					315					320
Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu	Gln	Thr	Leu	Leu	Lys	Tyr	Gly	Ile
				325					330					335	
Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys	Pro	Gln	Ala	Phe	Leu	Asn	Ser	Lys
			340				345						350		
Phe	Ser	Ile	Pro	Ala	Tyr	Lys	Leu	Ser	Asn	Pro	Thr	Lys	Thr	Asp	Thr
	355						360					365			
Gly	Val	Tyr	Val	Glu	Ala	Ile	His	Asp	Ile	Gly	Asp	Phe	Thr	Leu	Thr
	370					375					380				
Gly	Gly	Leu	Arg	Tyr	Asp	Arg	Phe	Lys	Val	Lys	Thr	His	Asp	Gly	Arg
385					390					395					400
Thr	Val	Ser	Ser	Ser	Asn	Leu	Asn	Pro	Ser	Phe	Gly	Val	Ile	Trp	Gln
				405					410					415	
Pro	His	Glu	His	Trp	Ser	Phe	Ser	Ala	Ser	His	Asn	Tyr	Ala	Ser	Arg
			420				425						430		
Ser	Pro	Arg	Leu	Tyr	Asp	Ala	Leu	Gln	Thr	His	Gly	Lys	Arg	Gly	Ile
		435					440					445			
Ile	Ser	Ile	Ala	Asp	Gly	Thr	Lys	Ala	Glu	Arg	Ala	Arg	Asn	Thr	Glu
	450					455					460				
Ile	Gly	Phe	Asn	Tyr	Asn	Asp	Gly	Thr	Phe	Ala	Ala	Asn	Gly	Ser	Tyr
465					470					475					480
Phe	Trp	Gln	Thr	Ile	Lys	Asp	Ala	Leu	Ala	Asn	Pro	Gln	Asn	Arg	His
				485					490					495	
Asp	Ser	Val	Ala	Val	Arg	Glu	Ala	Val	Asn	Ala	Gly	Tyr	Ile	Lys	Asn
			500					505					510		
His	Gly	Tyr	Glu	Leu	Gly	Ala	Ser	Tyr	Arg	Thr	Gly	Gly	Leu	Thr	Ala
		515					520					525			
Lys	Val	Gly	Val	Ser	His	Ser	Lys	Pro	Arg	Phe	Tyr	Asp	Thr	His	Lys
	530					535					540				
Asp	Lys	Leu	Leu	Ser	Ala	Asn	Pro	Glu	Phe	Gly	Ala	Gln	Val	Gly	Arg
545					550					555					560
Thr	Trp	Thr	Ala	Ser	Leu	Ala	Tyr	Arg	Phe	Gln	Asn	Pro	Asn	Leu	Glu
				565					570					575	
Ile	Gly	Trp	Arg	Gly	Arg	Tyr	Val	Gln	Lys	Ala	Thr	Gly	Ser	Ile	Leu
			580					585					590		
Ala	Ala	Gly	Gln	Lys	Asp	Arg	Lys	Gly	Asn	Leu	Glu	Asn	Val	Val	Arg
		595					600					605			
Lys	Gly	Phe	Gly	Val	Asn	Asp	Val	Phe	Ala	Asn	Trp	Lys	Pro	Leu	Gly
	610					615					620				
Lys	Asp	Thr	Leu	Asn	Val	Asn	Leu	Ser	Val	Asn	Asn	Val	Phe	Asn	Lys
625					630					635					640

Phe Tyr Tyr Pro His Ser Gln Arg Trp Thr Asn Thr Leu Pro Gly Val
645 650 655
Gly Arg Asp Val Arg Leu Gly Val Asn Tyr Lys Phe
660 665

<210> 30
<211> 2328
<212> DNA
<213> Artificial Sequence

<220>
<223> Meningococcal frpB with inner-core LOS binding
sequence (EVLFRGT) built into a loop

<400> 30
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ttggatttac ttcccttcat actcaagagg acgattgaat gaatacccca ttgttccgtc 120
tcagcctgct ctccgtcaca cttgcggcag gttttgccc cgcggcagaa aataatgcca 180
aggctcgact ggataccggt actgtaaaag gcgaccgcca aggcagcaaa atccgtacca 240
acatcggttac gctgcaacaa aaagacgaaa gcaccgcaac cgatatgcgc gaactcttaa 300
aagaagagcc gtccatcgat ttccggcgcg gcaacggcac gtcccaattc ctgacgctgc 360
gcggcatggg tcagaactct gtcgacatca aggtggacaa cgcctattcc gacagccaaa 420
tcctttacca ccaaggcaga tttattgtcg atcccgttt ggtaaagtc gtttccgtac 480
aaaaaggcgc gggttccgcc tctgccggta tcggcgcgac caacggcgcg atcatcgcca 540
aaaccgtcga tgcccaagac ctgctcaaag gcttggataa aaactggggc gtgcgcctca 600
acagcggctt tgccagcaac gaaggcgtaa gctacggcgc aagcgtattc ggaaaagagg 660
gcaacttcga cggcttgctt tcttacaacc gcaacgatga aaaagattac gaagccggca 720
aaggtttccg caatgtcaac ggcggaacaa ccgtaccgta cagcgcgctg gacaaacgca 780
gctacctcgc caaaatcgga acaaccttcg gcgacgacga ccaccgcac gtgttgagcc 840
acatgaaaga ccaacaccgg ggcatccgca ctgtgcgtga agaatttacc gtccggcgaca 900
aaagttcacg gataaatatt gaccgccaag cccctgctta ccgcgaaact acccaatcca 960
acaccaactt ggcgtacacg ggtaaaaacc tgggctttgt cgaaaaactg gatgccaacg 1020
cctatgtgtt ggaaaaagaa cgctattccg ccgatgacag cggcaccggc tacgcaggca 1080
atgtaaaagg ccccaaccat acccgaatca ccaactcgtg tgcaacttc aacttcgaca 1140
gccgccttgc cgaacaaacc ctggtgaaat acggtatcaa ctaccgccat caggaaatca 1200
aaccgcaagc atttttgaac tcgaaattct ccattcccgc gacagaagag aaaaacggct 1260
aaaaagtcga tgaagtctta tttcgtggca cgaaaccgat ggaacaacaa atgaaagacc 1320
gtgcagatga agacactgtt cagccctaca aactttccaa cccgaccaa accgataccg 1380
gcgtatatgt tgaagccatt cagcactcgc gcgatttcac gctgaccggc gggctgcgtt 1440
acgaccgctt caaggtgaaa acccatgacg gcaaaaccgt ttcaagcagc aaccttaacc 1500
cgagtttcgg tgtgatttgg cagccgcacg aacactggag cttcagcgcg agccacaact 1560
acgccagccg cagcccgcg cgtgatgacg cgctgcaaac ccacggtaaa cgcggcatca 1620
tctcgattgc cgacggcaca aaagccgaac gcgcgcgcaa taccgaaatc ggcttcaact 1680
acaacgacgc cagttttgcc gcaaacggca gctacttctg gcagaccatc aaagacgcgc 1740
ttgccaatcc gcaaaaccgc cagcactctg tcgccgtccg tgaagccgtc aatgccggtt 1800
acatcaaaaa ccacggttac gaattgggcg cgtcctaccg caccggcggc ctgactgcca 1860
aagtcggcgt cagccacagc aaaccgcgct ttacgatac gcacaaagac aagctgttga 1920
gcgcgaatcc tgaatttggc gcacaagtcg gccgcacttg gacggcctcc cttgcctacc 1980
gcttccaaaa tccgaatctg gaaatcggct ggcgcgccg ttatgttcaa aaagctacgg 2040
gttcgatatt ggcggcaggt caaaaagacc gcaaaaggcaa cttggaaaac gttgtacgca 2100
aaggtttcgg tgtgaacgat gtcttcgcca actggaaacc gctgggcaaa gacacgctca 2160
atgtcaatct ttcggttaac aacgtgttca acaagttcta ctatccgcac agccaacgct 2220
ggaccaatac cctgccgggc gtgggacgtg atgtacgctt gggcgtgaac tacaagttct 2280
aaaacgcaca tcccgaaaaa atgccgtctg aaagcctttc agacggca 2328

<210> 31
<211> 727
<212> PRT
<213> Artificial Sequence

<220>

<223> Meningococcal frpB with inner-core LOS binding
sequence (EVLFRGT) built into a loop

<400> 31

Met	Asn	Thr	Pro	Leu	Phe	Arg	Leu	Ser	Leu	Leu	Ser	Leu	Thr	Leu	Ala
1				5					10					15	
Ala	Gly	Phe	Ala	His	Ala	Ala	Glu	Asn	Asn	Ala	Lys	Val	Val	Leu	Asp
			20					25					30		
Thr	Val	Thr	Val	Lys	Gly	Asp	Arg	Gln	Gly	Ser	Lys	Ile	Arg	Thr	Asn
		35					40					45			
Ile	Val	Thr	Leu	Gln	Gln	Lys	Asp	Glu	Ser	Thr	Ala	Thr	Asp	Met	Arg
	50					55					60				
Glu	Leu	Leu	Lys	Glu	Glu	Pro	Ser	Ile	Asp	Phe	Gly	Gly	Gly	Asn	Gly
65					70					75				80	
Thr	Ser	Gln	Phe	Leu	Thr	Leu	Arg	Gly	Met	Gly	Gln	Asn	Ser	Val	Asp
			85						90					95	
Ile	Lys	Val	Asp	Asn	Ala	Tyr	Ser	Asp	Ser	Gln	Ile	Leu	Tyr	His	Gln
			100					105					110		
Gly	Arg	Phe	Ile	Val	Asp	Pro	Ala	Leu	Val	Lys	Val	Val	Ser	Val	Gln
		115					120					125			
Lys	Gly	Ala	Gly	Ser	Ala	Ser	Ala	Gly	Ile	Gly	Ala	Thr	Asn	Gly	Ala
	130					135					140				
Ile	Ile	Ala	Lys	Thr	Val	Asp	Ala	Gln	Asp	Leu	Leu	Lys	Gly	Leu	Asp
145					150					155				160	
Lys	Asn	Trp	Gly	Val	Arg	Leu	Asn	Ser	Gly	Phe	Ala	Ser	Asn	Glu	Gly
			165						170					175	
Val	Ser	Tyr	Gly	Ala	Ser	Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly
			180					185					190		
Leu	Phe	Ser	Tyr	Asn	Arg	Asn	Asp	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys
		195				200						205			
Gly	Phe	Arg	Asn	Val	Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu
	210					215					220				
Asp	Lys	Arg	Ser	Tyr	Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Asp
225					230					235				240	
Asp	His	Arg	Ile	Val	Leu	Ser	His	Met	Lys	Asp	Gln	His	Arg	Gly	Ile
			245						250					255	
Arg	Thr	Val	Arg	Glu	Glu	Phe	Thr	Val	Gly	Asp	Lys	Ser	Ser	Arg	Ile
		260						265					270		
Asn	Ile	Asp	Arg	Gln	Ala	Pro	Ala	Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn
	275					280						285			
Thr	Asn	Leu	Ala	Tyr	Thr	Gly	Lys	Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu
290					295						300				
Asp	Ala	Asn	Ala	Tyr	Val	Leu	Glu	Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp
305					310					315				320	
Ser	Gly	Thr	Gly	Tyr	Ala	Gly	Asn	Val	Lys	Gly	Pro	Asn	His	Thr	Arg
			325						330					335	
Ile	Thr	Thr	Arg	Gly	Ala	Asn	Phe	Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu
		340						345					350		
Gln	Thr	Leu	Leu	Lys	Tyr	Gly	Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys
	355					360						365			
Pro	Gln	Ala	Phe	Leu	Asn	Ser	Lys	Phe	Ser	Ile	Pro	Thr	Thr	Glu	Glu
	370				375						380				
Lys	Asn	Gly	Gln	Lys	Val	Asp	Glu	Val	Leu	Phe	Arg	Gly	Thr	Lys	Pro
385					390					395				400	
Met	Glu	Gln	Gln	Met	Lys	Asp	Arg	Ala	Asp	Glu	Asp	Thr	Val	His	Ala
			405						410					415	
Tyr	Lys	Leu	Ser	Asn	Pro	Thr	Lys	Thr	Asp	Thr	Gly	Val	Tyr	Val	Glu
		420						425					430		
Ala	Ile	His	Asp	Ile	Gly	Asp	Phe	Thr	Leu	Thr	Gly	Gly	Leu	Arg	Tyr

[illegible]